

Molecular Characterization of Major Isolated Organism Involved in Bovine Subclinical Mastitis

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Abstract : Mastitis is a common problem of dairy industries. Reduction in milk production and an irreparable damage to the udder associated with the disease are common causes of culling of dairy cows. Milk from infected animals is not suitable for drinking and for making different milk products. So, it has a major economic importance in dairy cattle. The aims of this study were to investigate the bacteriological panorama in milk from udder quarters with subclinical mastitis and to carried out for the molecular characterization of the major isolated organisms, from subclinical mastitis-affected cows in and around Durg and Rajnandgaon district of Chhattisgarh. Isolation and identification of bacteria from the milk samples of subclinical mastitis-affected cows were done by standard and routine culture procedures. A total of 78 isolates were obtained from cows and among the various bacteria isolated, Staphylococcus spp. occupied prime position with occurrence rate of 51.282%. However, other bacteria isolated include Streptococcus spp. (20.512%), Micrococcus spp. (14.102%), E. coli (8.974%), Klebsiella spp. (2.564%), Salmonella spp. (1.282%) and Proteus spp. (1.282%). Staphylococcus spp. was isolated as the major causative agent of subclinical mastitis in the studied area. Molecular characterization of Staphylococcus aureus isolates was done for genetic expression of the virulence genes like 'nuc' encoding thermonuclease exoenzyme, coa and spa by PCR amplification of the respective genes in 25 Staphylococcus isolates. In the present study, 15 isolates (77.27%) out of 20 coagulase positive isolates were found to be genotypically positive for 'nuc' where as 20 isolates (52.63%) out of 38 CNS expressed the presence of the same virulence gene. In the present study, three Staphylococcus isolates were found to be genotypically positive for coa gene. The Amplification of the coa gene yielded two different products of 627, 710 bp. The amplification of the gene segment encoding the IgG binding region of protein A (spa) revealed a size of 220 and 253bp in two staphylococcus isolates. The X-region binding of the spa gene produced an amplicon of 315 bp in one Staphylococcal isolates. Staphylococcus aureus was found to be major isolate (51.28%) responsible for causing subclinical mastitis in cows which also showed expression of virulence genes nuc, coa and spa.

Keywords : mastitis, bacteria, characterization, expression, gene

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